

#9

1638

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/508,710

DATE: 02/27/2001  
TIME: 10:15:25

Input Set : A:\SN09508710seqlist.txt  
Output Set: N:\CRF3\02272001\I508710.raw

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```

4 <110> APPLICANT: Cole, David
5      Cummins, Ian
6      Edwards, Robert
8 <120> TITLE OF INVENTION: Plant Genes
11 <130> FILE REFERENCE: A33083-PCT-USA 072667.0127
13 <140> CURRENT APPLICATION NUMBER: 09/508,710
14 <141> CURRENT FILING DATE: 2000-07-10
16 <150> PRIOR APPLICATION NUMBER: PCT/GB98/02802
17 <151> PRIOR FILING DATE: 1998-09-16
19 <150> PRIOR APPLICATION NUMBER: GB 971972.1
20 <151> PRIOR FILING DATE: 1997-09-16
22 <160> NUMBER OF SEQ ID NOS: 19
24 <170> SOFTWARE: FastSEQ for Windows Version 3.0
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 1085
28 <212> TYPE: DNA
29 <213> ORGANISM: Triticum aestivum L.
31 <220> FEATURE:
32 <221> NAME/KEY: CDS
33 <222> LOCATION: (46)...(711)
34 <223> OTHER INFORMATION: Glutathione S transferase
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37 caaacacaag cacagatcgg tcgagattca aggcacccgg gagca atg gcg ggc gag      57
38                                     Met Ala Gly Glu
39                                     1
41 aag ggg ctg gtg ctg ctg gac ttc tgg gtg agc ccg ttc ggg cag cgc      105
42 Lys Gly Leu Val Leu Leu Asp Phe Trp Val Ser Pro Phe Gly Gln Arg
43   5                               10                               20
45 gtg cgc atc gcg ctg gcc gag aag ggc ctg ccc tac gag tac gcg gag      153
46 Val Arg Ile Ala Leu Ala Glu Lys Gly Leu Pro Tyr Glu Tyr Ala Glu
47   25                               30                               35
49 gag gac ctg atg gcc ggc aag agc gac cgc ctc ctc cgc gcc aac ccg      201
50 Glu Asp Leu Met Ala Gly Lys Ser Asp Arg Leu Leu Arg Ala Asn Pro
51   40                               45                               50
53 gtg cat aag aag atc ccg gtg ctc ctc cac gac ggc cgt gcc gtc aac      249
54 Val His Lys Lys Ile Pro Val Leu Leu His Asp Gly Arg Ala Val Asn
55   55                               60                               65
57 gag tcc ctc atc atc ctc cag tac ctg gag gag gcc ttc ccg gac gcg      297
58 Glu Ser Leu Ile Ile Leu Gln Tyr Leu Glu Glu Ala Phe Pro Asp Ala
59   70                               75                               80
61 ccc gct ctg ctc ccc tcc gac ccc tac gcg cgc gcg cag gcc cgc ttc      345
62 Pro Ala Leu Leu Pro Ser Asp Pro Tyr Ala Arg Ala Gln Ala Arg Phe
63   85                               90                               95                               100
65 tgg gcc gac tac gtc gac aag aag gtc tac gac tgc ggc tcc cgc ctc      393
66 Trp Ala Asp Tyr Val Asp Lys Lys Val Tyr Asp Cys Gly Ser Arg Leu
67   105                               110                               115
69 tgg aag ctc aag ggc gag ccg cag gcg cag gcg cgc gcc gag atg ctg      441

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70 Trp Lys Leu Lys Gly Glu Pro Gln Ala Gln Ala Arg Ala Glu Met Leu
71      120      125      130
73 gac atc ctc aag acc ctc gac ggc gcg ctc ggc gac aag ccc ttc ttc 489
74 Asp Ile Leu Lys Thr Leu Asp Gly Ala Leu Gly Asp Lys Pro Phe Phe
75      135      140      145
77 ggc ggc gac aag ttc ggc ttc gtc gac gcc gcc ttc gcg ccc ttc acc 537
78 Gly Gly Asp Lys Phe Gly Phe Val Asp Ala Ala Phe Ala Pro Phe Thr
79      150      155      160
81 gcg tgg ttc cac agc tac gag agg tac ggc gag ttc agc ctg ccg gag 585
82 Ala Trp Phe His Ser Tyr Glu Arg Tyr Gly Glu Phe Ser Leu Pro Glu
83      165      170      175      180
85 ttc gcg ccc aag atc gcc gcg tgg gcc aag cgc tgc ggc gag ccg gag 633
86 Val Ala Pro Lys Ile Ala Ala Trp Ala Lys Arg Cys Gly Glu Arg Glu
87      185      190      195
89 agc gtc gcc aag agc ctc tac tcy ccg gac aag gtg tac gac ttc atc 681
90 Ser Val Ala Lys Ser Leu Tyr Ser Pro Asp Lys Val Tyr Asp Phe Ile
91      200      205      210
93 ggc ctg ctc aag aag aag tac ggc atc gag tagggcgcc gacggacgga 731
94 Gly Leu Leu Lys Lys Lys Tyr Gly Ile Glu
95      215      220
97 cggacgggcc atgcagcga cagccggccc gccgtccgga gggaagcaac aaataaatca 791
98 gggagcgatt tgggtggcct acaatgcgta cgtctggata gagtatttct ttctttcttt 851
99 cttcgtggaa taaagtgtc cgtgtgtgtg tgggtgggtg ttgttgggtg gatcagtcag 911
100 tgtgtgtggg tgcgtgttgt gtactcagta ctctgtatgt gtgtgtgtgt caatgtgtca 971
101 accctggctt tcggtgggg cagcaccgag ttccaccctg ccattccatt tccattccg 1031
102 gcgatgaata aattaaaaaa .gagtcctcatt tgtttaaaaa aaaaaaaaaa aaaa 1085
104 <210> SEQ ID NO: 2
105 <211> LENGTH: 222
106 <212> TYPE: PRT
107 <213> ORGANISM: Triticum aestivum L.
109 <400> SEQUENCE: 2
110 Met Ala Gly Glu Lys Gly Leu Val Leu Leu Asp Phe Trp Val Ser Pro
111      1      5      10      15
112 Phe Gly Gln Arg Val Arg Ile Ala Leu Ala Glu Lys Gly Leu Pro Tyr
113      20      25      30
114 Glu Tyr Ala Glu Glu Asp Leu Met Ala Gly Lys Ser Asp Arg Leu Leu
115      35      40      45
116 Arg Ala Asn Pro Val His Lys Lys Ile Pro Val Leu Leu His Asp Gly
117      50      55      60
118 Arg Ala Val Asn Glu Ser Leu Ile Ile Leu Gln Tyr Leu Glu Glu Ala
119      65      70      75      80
120 Phe Pro Asp Ala Pro Ala Leu Leu Pro Ser Asp Pro Tyr Ala Arg Ala
121      85      90      95
122 Gln Ala Arg Phe Trp Ala Asp Tyr Val Asp Lys Lys Val Tyr Asp Cys
123      100      105      110
124 Gly Ser Arg Leu Trp Lys Leu Lys Gly Glu Pro Gln Ala Gln Ala Arg
125      115      120      125
126 Ala Glu Met Leu Asp Ile Leu Lys Thr Leu Asp Gly Ala Leu Gly Asp
127      130      135      140

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```

128 Lys Pro Phe Phe Gly Gly Asp Lys Phe Gly Phe Val Asp Ala Ala Phe
129 145 150 155 160
130 Ala Pro Phe Thr Ala Trp Phe His Ser Tyr Glu Arg Tyr Gly Glu Phe
131 165 170 175
132 Ser Leu Pro Glu Val Ala Pro Lys Ile Ala Ala Trp Ala Lys Arg Cys
133 180 185 190
134 Gly Glu Arg Glu Ser Val Ala Lys Ser Leu Tyr Ser Pro Asp Lys Val
135 195 200 205
136 Tyr Asp Phe Ile Gly Leu Leu Lys Lys Tyr Gly Ile Glu
137 210 215 220
139 <210> SEQ ID NO: 3
140 <211> LENGTH: 865
141 <212> TYPE: DNA
142 <213> ORGANISM: Triticum aestivum L.
144 <220> FEATURE:
145 <221> NAME/KEY: CDS
146 <222> LOCATION: (54)...(725)
147 <223> OTHER INFORMATION: WIC 1
149 <400> SEQUENCE: 3
150 ggaactcaac cattgatctt caagaagcgg aagcaaacag agcaaaaggt gtg atg 56
151 Met
152 1
154 gcg gcg ccg gcg gtg aag gtg tac qgg tgg gcg atg tcg ccg ttc gtg 104
155 Ala Ala Pro Ala Val Lys Val Tyr Gly Trp Ala Met Ser Pro Phe Val
156 5 10 15
158 gcg cgc gcg ctg ctg tgc ctg gag gag gcc gcc gtg gag tac gag ctc 152
159 Ala Arg Ala Leu Leu Cys Leu Glu Glu Ala Gly Val Glu Tyr Glu Leu
160 20 25 30
162 gtc ccc atg agc cgc gag gcc gcc gac cac cgc cag ccc gac ttc ctc 200
163 Val Pro Met Ser Arg Glu Ala Gly Asp His Arg Gln Pro Asp Phe Leu
164 35 40 45
166 gcc cgg aac ccc ttc gcc cag gtc ccc gtt ctc qag gac gcc gac ctc 248
167 Ala Arg Asn Pro Phe Gly Gln Val Pro Val Leu Glu Asp Gly Asp Leu
168 50 55 60 65
170 acc atc ttc gag tcg cgc gcc gtc gcg agg cac gtg ctg cgc aag cac 296
171 Thr Ile Phe Glu Ser Arg Ala Val Ala Arg His Val Leu Arg Lys His
172 70 75 80
174 aaa ccg gag ctg ctg gcc tcc gcc tcg ccg gag tcg gcg gcg atg gtg 344
175 Lys Pro Glu Leu Leu Gly Ser Gly Ser Pro Glu Ser Ala Ala Met Val
176 85 90 95
178 gac gtg tgg ctg gag gtg gag gcc cac cag cac cag acc ccg gcg gcc 392
179 Asp Val Trp Leu Glu Val Glu Ala His Gln His Gln Thr Pro Ala Gly
180 100 105 110
182 acc atc gtc atg cag tgc atc ctc acc ccg ttc ctc gcc tgc cag cgc 440
183 Thr Ile Val Met Gln Cys Ile Leu Thr Pro Phe Leu Gly Cys Gln Arg
184 115 120 125
186 gac cag gcc gcc atc gac gag aac gcg gca aag ctg acg aat ctg ttc 488
187 Asp Gln Ala Ala Ile Asp Glu Asn Ala Ala Lys Leu Thr Asn Leu Phe
188 130 135 140 145

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190 gac gtg tac gag gcg cgc ctg tcg gcg tcg agg tac ctt gcc ggg gag      536
191 Asp Val Tyr Glu Ala Arg Leu Ser Ala Ser Arg Tyr Leu Ala Gly Glu
192                               150                               155                               160
194 gcg gtc agc ctc gcg gac ctc agc cac ttc ccg ttc atg cga tac ttc      584
195 Ala Val Ser Leu Ala Asp Leu Ser His Phe Pro Phe Met Arg Tyr Phe
196                               165                               170                               175
198 atg gac acc gag tac gcg tcg ctg glg gag gag cgc ccg cac gtg aag      632
199 Met Asp Thr Glu Tyr Ala Ser Leu Val Glu Glu Arg Pro His Val Lys
200                               180                               185                               190
202 gcg tgg tgg gag gag ttc aag gcc agc ccg gcg gcg aag agg gtg acg      680
203 Ala Trp Trp Glu Glu Phe Lys Ala Ser Pro Ala Ala Lys Arg Val Thr
204                               195                               200                               205
206 gag ttc atg ccg cca aac ttc ggg ttc gga aag aag gca gag aag      725
207 Glu Phe Met Pro Pro Asn Phe Gly Phe Gly Lys Lys Ala Glu Lys
208                               210                               215                               220
210 tgatgacaag aacgaacacc gagcgaacat gttgtgtggt ctgtgcgacc cgaccatggc      785
211 tcaatgtttt gggctgtttt tgtttcacgc atgaatgaat aaaaacaaat gcttttgggt      845
212 ttcaaaaaaa aaaaaaa      865
214 <210> SEQ ID NO: 4
215 <211> LENGTH: 224
216 <212> TYPE: PRT
217 <213> ORGANISM: Triticum aestivum L.
219 <400> SEQUENCE: 4
220 Met Ala Ala Pro Ala Val Lys Val Tyr Gly Trp Ala Met Ser Pro Phe
221 1 5 10 15
222 Val Ala Arg Ala Leu Leu Cys Leu Glu Glu Ala Gly Val Glu Tyr Glu
223 20 25 30
224 Leu Val Pro Met Ser Arg Glu Ala Gly Asp His Arg Gln Pro Asp Phe
225 35 40 45
226 Leu Ala Arg Asn Pro Phe Gly Gln Val Pro Val Leu Glu Asp Gly Asp
227 50 55 60
228 Leu Thr Ile Phe Glu Ser Arg Ala Val Ala Arg His Val Leu Arg Lys
229 65 70 75 80
230 His Lys Pro Glu Leu Leu Gly Ser Gly Ser Pro Glu Ser Ala Ala Met
231 85 90 95
232 Val Asp Val Trp Leu Glu Val Glu Ala His Gln His Gln Thr Pro Ala
233 100 105 110
234 Gly Thr Ile Val Met Gln Cys Ile Leu Thr Pro Phe Leu Gly Cys Gln
235 115 120 125
236 Arg Asp Gln Ala Ala Ile Asp Glu Asn Ala Ala Lys Leu Thr Asn Leu
237 130 135 140
238 Phe Asp Val Tyr Glu Ala Arg Leu Ser Ala Ser Arg Tyr Leu Ala Gly
239 145 150 155 160
240 Glu Ala Val Ser Leu Ala Asp Leu Ser His Phe Pro Phe Met Arg Tyr
241 165 170 175
242 Phe Met Asp Thr Glu Tyr Ala Ser Leu Val Glu Glu Arg Pro His Val
243 180 185 190
244 Lys Ala Trp Trp Glu Glu Phe Lys Ala Ser Pro Ala Ala Lys Arg Val
245 195 200 205

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246 Thr Glu Phe Met Pro Pro Asn Phe Gly Phe Gly Lys Lys Ala Glu Lys
247      210                      215                      220
249 <210> SEQ ID NO: 5
250 <211> LENGTH: 930
251 <212> TYPE: DNA
252 <213> ORGANISM: Triticum aestivum L.
254 <220> FEATURE:
255 <221> NAME/KEY: CDS
256 <222> LOCATION: (60)...(725)
257 <223> OTHER INFORMATION: WIC 2
259 <400> SEQUENCE: 5
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261 atg gcg ccg gcg gtg aag gtg tac ggg tgg gcc gtg tcg ccg ttc gtg      107
262 Met Ala Pro Ala Val Lys Val Tyr Gly Trp Ala Val Ser Pro Phe Val
263      1                      5                      10                      15
265 gcg cgc cca ctg ctg tgc ctg gag gag gcc gcc gtc gag tac gag ctg      155
266 Ala Arg Pro Leu Leu Cys Leu Glu Glu Ala Gly Val Glu Tyr Glu Leu
267      20                      25                      30
269 gtg tcc atg agc cgc gcg gcc ggc gac cac cgc cag ccg gac ttc ctg      203
270 Val Ser Met Ser Arg Ala Ala Gly Asp His Arg Gln Pro Asp Phe Leu
271      35                      40                      45
273 gcc cgg aac ccc ttc ggc cag gtc ccc gtc ctg gag gac ggc gac ctg      251
274 Ala Arg Asn Pro Phe Gly Gln Val Pro Val Leu Glu Asp Gly Asp Leu
275      50                      55                      60
277 acc ctg ttc gag tcg cgc gcg atc gcg agg cac gtg ctg ccg aag cac      299
278 Thr Leu Phe Glu Ser Arg Ala Ile Ala Arg His Val Leu Arg Lys His
279      65                      70                      75                      80
281 aag ccg gag ctg ctg ggc tgc ggc tcg ccg gag gcg gag gcg atg gtg      347
282 Lys Pro Glu Leu Leu Gly Cys Gly Ser Pro Glu Ala Glu Ala Met Val
283      85                      90                      95
285 gac gtg tgg ctg gag gtg gag gcc cac cag tac aac ccc gcg gcc agc      395
286 Asp Val Trp Leu Glu Val Glu Ala His Gln Tyr Asn Pro Ala Ala Ser
287      100                      105                      110
289 gcc atc gtg gtg cag tgc atc atc ttg ccg cta ctg ggc ggc gcg ccg      443
290 Ala Ile Val Val Gln Cys Ile Ile Leu Pro Leu Leu Gly Gly Ala Arg
291      115                      120                      125
293 gac cag gcg gtg gtg gac gag aac gta gcc aag ctg aag aag gtg ctg      491
294 Asp Gln Ala Val Val Asp Glu Asn Val Ala Lys Leu Lys Lys Val Leu
295      130                      135                      140
297 gag gtg tac gag gca cgg ctg tcg gcg tcc agg tac ctg gcc ggg gac      539
298 Glu Val Tyr Glu Ala Arg Leu Ser Ala Ser Arg Tyr Leu Ala Gly Asp
299      145                      150                      155                      160
301 gac atc agc ctg gcc gac ctg agc cac ttc ccc ttc acg cgc tac ttc      587
302 Asp Ile Ser Leu Ala Asp Leu Ser His Phe Pro Phe Thr Arg Tyr Phe
303      165                      170                      175
305 atg gag acg gag tac gcg ccg ctg gtg gcg gag ctg ccc cac gtg aac      635
306 Met Glu Thr Glu Tyr Ala Pro Leu Val Ala Glu Leu Pro His Val Asn
307      180                      185                      190
309 gcg tgg tgg gag ggg ctg aag gcc agg ccg gcc gcg agg aag gtg acg      683

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VERIFICATION SUMMARY                      DATE: 02/27/2001  
PATENT APPLICATION:    US/09/508,710        TIME: 10:15:26  
  
Input Set : A:\SN09508710seqlist.txt  
Output Set: N:\CRF3\02272001\I508710.raw